

# SEQUENCE LISTING

<110> Rosanne M. Crooke  
Mark J. Graham  
Kristina M. Lemonidis

<120> ANTISENSE MODULATION OF ACYL COA CHOLESTEROL ACYLTRANSFERASE-2  
EXPRESSION

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<213> Homo sapiens

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1				5					10					15		

gga	ggg	gag	cgg	gag	cgc	caa	ccc	tgt	gga	gat	gga	aac	act	gag	acg	96
Gly	Gly	Glu	Arg	Glu	Arg	Gln	Pro	Cys	Gly	Asp	Gly	Asn	Thr	Glu	Thr	
			20					25					30			

cac	aga	gcc	ccg	gac	ttg	gta	caa	tgg	acc	cga	cac	atg	gag	gct	gtg	144
His	Arg	Ala	Pro	Asp	Leu	Val	Gln	Trp	Thr	Arg	His	Met	Glu	Ala	Val	





tac gca cgg cgg cac tgc ccc tta ccc cag gca act ttc tgg ggg ctg	1536
Tyr Ala Arg Arg His Cys Pro Leu Pro Gln Ala Thr Phe Trp Gly Leu	
500 505 510	

gtg aca cct cga tct tgg tcc tgc cat acc tag	1569
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 1 5

cgg agg aga gaa ggg ctg gga gag gag cag gag aag gga gcc cgt gga 101  
 Arg Arg Arg Glu Gly Leu Gly Glu Glu Gln Glu Lys Gly Ala Arg Gly  
 10 15 20

gga gaa ggg aac gca agg aca cac gga acc cca gac ttg gtg caa tgg 149  
 Gly Glu Gly Asn Ala Arg Thr His Gly Thr Pro Asp Leu Val Gln Trp  
 25 30 35 40

act cga cat atg gag gct gtg aag acn cag ttt ctg gag caa gca cag 197  
 Thr Arg His Met Glu Ala Val Lys Thr Gln Phe Leu Glu Gln Ala Gln  
 45 50 55

aga gag ttg gca gag ctg ttg gat cgg gcc cta tgg gag gct atg caa 245  
 Arg Glu Leu Ala Glu Leu Leu Asp Arg Ala Leu Trp Glu Ala Met Gln  
 60 65 70

gct tac ccc aaa caa gac aga cct ctt ccc tcc gct gcc cca gat tct 293  
 Ala Tyr Pro Lys Gln Asp Arg Pro Leu Pro Ser Ala Ala Pro Asp Ser  
 75 80 85

aca agc aag acc ccg gag tta cgc cct gga aaa cgg aaa gtt ttc gtc 341  
 Thr Ser Lys Thr Pro Glu Leu Arg Pro Gly Lys Arg Lys Val Phe Val  
 90 95 100

gcc cgc aag tca ctg atc gat gag cta atg gag gtg caa cat ttc cga 389

Ala	Arg	Lys	Ser	Leu	Ile	Asp	Glu	Leu	Met	Glu	Val	Gln	His	Phe	Arg		
105					110					115					120		
acc	atc	tac	cac	atg	ttc	ata	gcg	ggc	cta	tgg	ttc	ttg	atc	atc	agc	437	
Thr	Ile	Tyr	His	Met	Phe	Ile	Ala	Gly	Leu	Trp	Phe	Leu	Ile	Ile	Ser		
				125					130						135		
acc	ctg	gcc	atc	gac	ttc	att	gat	gag	ggc	agg	ttg	atg	ctg	gag	ttt	485	
Thr	Leu	Ala	Ile	Asp	Phe	Ile	Asp	Glu	Gly	Arg	Leu	Met	Leu	Glu	Phe		
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gac	tta	ctc	ctc	ttc	agc	ttc	gga	cag	ctg	ccc	ttg	gcg	ctg	atg	acc	533	
Asp	Leu	Leu	Leu	Phe	Ser	Phe	Gly	Gln	Leu	Pro	Leu	Ala	Leu	Met	Thr		
		155					160					165					
tgg	gtt	ccc	atg	ttc	ctg	tat	acg	ctc	cta	gtg	ccc	tac	cag	acc	ctg	581	
Trp	Val	Pro	Met	Phe	Leu	Tyr	Thr	Leu	Leu	Val	Pro	Tyr	Gln	Thr	Leu		
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tgg	ctg	tgg	gcc	agg	ccg	cgc	gct	ggg	ggt	gcc	tgg	atg	ctg	ggg	gcc	629	
Trp	Leu	Trp	Ala	Arg	Pro	Arg	Ala	Gly	Gly	Ala	Trp	Met	Leu	Gly	Ala		
	185				190					195					200		
agc	ctg	ggc	tgc	gtt	ctg	ctg	gct	gcc	cac	gct	gtg	gtg	ctc	tgc	gtc	677	
Ser	Leu	Gly	Cys	Val	Leu	Leu	Ala	Ala	His	Ala	Val	Val	Leu	Cys	Val		
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ctg	ccg	gtg	cac	gtg	tca	gtg	agg	cat	gag	ctt	ccg	ccc	gcc	tgc	cgc	725	
Leu	Pro	Val	His	Val	Ser	Val	Arg	His	Glu	Leu	Pro	Pro	Ala	Ser	Arg		
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tgc	gtg	ctg	gtc	ttt	gag	cag	gtc	aga	ttg	ctg	atg	aaa	agc	tac	tcc	773	
Cys	Val	Leu	Val	Phe	Glu	Gln	Val	Arg	Leu	Leu	Met	Lys	Ser	Tyr	Ser		
		235					240					245					
ttc	ctg	aga	gag	act	gtg	cct	ggg	atc	ttt	tgt	gtc	aga	cga	gga	aag	821	
Phe	Leu	Arg	Glu	Thr	Val	Pro	Gly	Ile	Phe	Cys	Val	Arg	Arg	Gly	Lys		
		250				255					260						
ggc	atc	agc	ccc	cca	agt	ttc	tcc	agc	tac	ctc	tac	ttc	ctc	ttc	tgc	869	
Gly	Ile	Ser	Pro	Pro	Ser	Phe	Ser	Ser	Tyr	Leu	Tyr	Phe	Leu	Phe	Cys		
					270					275					280		
cct	aca	ctt	atc	tac	aga	gag	aca	tac	ccc	agg	aca	ccc	agc	atc	agg	917	
Pro	Thr	Leu	Ile	Tyr	Arg	Glu	Thr	Tyr	Pro	Arg	Thr	Pro	Ser	Ile	Arg		
				285					290					295			
tgg	aac	tat	gtg	gcc	aag	aac	ttt	gcc	cag	gtc	ctg	ggc	tgt	ttg	ctc	965	
Trp	Asn	Tyr	Val	Ala	Lys	Asn	Phe	Ala	Gln	Val	Leu	Gly	Cys	Leu	Leu		
			300					305					310				
tat	gcc	tgc	ttc	atc	ctg	ggc	cgc	ctc	tgt	gtc	cct	gtc	ttt	gcc	aac	1013	
Tyr	Ala	Cys	Phe	Ile	Leu	Gly	Arg	Leu	Cys	Val	Pro	Val	Phe	Ala	Asn		
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atg	agc	cgg	gaa	ccc	ttc	agc	acc	cgg	gct	ctg	ctg	ctc	tcc	atc	ttg	1061	
Met	Ser	Arg	Glu	Pro	Phe	Ser	Thr	Arg	Ala	Leu	Leu	Leu	Ser	Ile	Leu		

330	335	340	
cat gcc acg ggg cca ggc atc ttc atg ctg ctc ctc atc ttc ttc gcc			1109
His Ala Thr Gly Pro Gly Ile Phe Met Leu Leu Leu Ile Phe Phe Ala			
345	350	355	360
ttc ctg cac tgc tgg ctc aac gcc ttc gcc gag atg ctg cgg ttt gga			1157
Phe Leu His Cys Trp Leu Asn Ala Phe Ala Glu Met Leu Arg Phe Gly			
	365	370	375
gac agg atg ttc tac cgg gac tgg tgg aac tgc act tcc ttc tcc aac			1205
Asp Arg Met Phe Tyr Arg Asp Trp Trp Asn Ser Thr Ser Phe Ser Asn			
	380	385	390
tac tac cgc acc tgg aac gtc gtg gtc cat gac tgg ctg tac agc tat			1253
Tyr Tyr Arg Thr Trp Asn Val Val Val His Asp Trp Leu Tyr Ser Tyr			
	395	400	405
gtg tat caa gat ggg ctg tgg ctc tta ggc agg cgg gct cgc ggg gtg			1301
Val Tyr Gln Asp Gly Leu Trp Leu Leu Gly Arg Arg Ala Arg Gly Val			
	410	415	420
gcc atg ctg gga gtg ttc ctg gtg tct gcg gtg gtt cat gag tat atc			1349
Ala Met Leu Gly Val Phe Leu Val Ser Ala Val Val His Glu Tyr Ile			
	425	430	435
ttc tgc ttc gtc ctg ggg ttc ttc tac ccg gtc atg ctg atg cta ttc			1397
Phe Cys Phe Val Leu Gly Phe Phe Tyr Pro Val Met Leu Met Leu Phe			
	445	450	455
ctt gtt ttc ggg ggg ctg ctg aat ttc acc atg aac gac agg cac aca			1445
Leu Val Phe Gly Gly Leu Leu Asn Phe Thr Met Asn Asp Arg His Thr			
	460	465	470
ggt cca gcc tgg aac atc ctg atg tgg acc ttt ctc ttc atg ggc cag			1493
Gly Pro Ala Trp Asn Ile Leu Met Trp Thr Phe Leu Phe Met Gly Gln			
	475	480	485
ggc atc cag gtc agc cta tac tgc cag gag tgg tat gct cgt cga cac			1541
Gly Ile Gln Val Ser Leu Tyr Cys Gln Glu Trp Tyr Ala Arg Arg His			
	490	495	500
tgt ccc ctg ccc cag aca aca ttc tgg ggg atg gtg aca ccc caa tct			1589
Cys Pro Leu Pro Gln Thr Thr Phe Trp Gly Met Val Thr Pro Gln Ser			
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Trp Ser Cys His Thr			
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